

result No.	Score	Query Length	Match Length	DB	ID	Description
1	532.2	31.0	537	9	AW783013	AW783013 ra22d01.y
2	511.8	29.8	556	10	BE339174	BE239174 MD0830 Me
3	320.8	18.7	650	3	AW158739	MD152739 MALS08C01.y
4	301.4	17.5	327	9	AW589077	AW589077 ra08c01.y

SUMMARIES

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	532.2	31.0	537	9	AW73013	AW73013 ra22dd01 v
2	511.8	29.8	556	10	BE39174	BE229174 MD0830 Me
3	320.8	18.7	650	17	AW152139	AW152139 JALS1201 y
4	301.4	17.5	327	9	AW583077	AW583077 ra08C01 v

FEATURES		source	SEQUENCE	ORIGIN	Query Match	Best Local Similarity	DB 9;	Length
Seq. primer:	T3 ET	from Amer sham	537					
High quality sequence stop:	419.	Location/Qualifiers						
1.	• 537	/organism="Meloidogyne incognita"						
		/mol_type="mRNA"						
		/db_xref="taxon:6306"						
		/dev_stage="enriched for 2nd stage juveniles"						
		/lab_host="XORL"						
		/clone_id="Bird-Rao Meloidogyne incognita J2"						
		/note="Vector: ZAP express - pBRZM (Stratagene); Site 1: EcoRI; Site 2: XbaI; Oligo (dT) primed library. cDNA was constructed and cloned unidirectionally into the vector within the 5' EcoRI and 3' XbaI sites. This library was constructed by Dr. Uma Rao and Dr. David Bird at North Carolina State University."						
		152 a 92 c 123 g. 170 t						
SEQUENCE COUNT								
1					31.0%	Score 532.2;	DB 9;	Length 537;
2					99.4%	Pred. No. 1.2e-118;		
3					534; Conservative	0; Mismatches	3;	Indels 0; Gaps 0
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ACCESSION	BE229174	GI:	9034138
VERSION	BE229174.1		
KEYWORDS			
SOURCE	Meloidogyne incognita (southern root-knot nematode)		
ORGANISM	Meloidogyne incognita		
REFERENCE	Meloidogyne incognita; Nematoda; Chromadorea; Tylenchida; Tylenchidae; Meloidogyne; Meloidogyne; Tylenchoidea; Heteroderidae; Meloidogyinae; Meloidogyne.		
AUTHORS	Dautova, M., Gommers, F.J., Bakker, J. and Smant, G.		
TITLE	5', end expressed sequence tags from Meloidogyne incognita preparasitic J2 cDNA library		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Smant G / Dautova M Laboratory of Nematology Wageningen University and Research Center Box 8123, Binnenhaven 10, 6709 PD Wageningen, The Netherlands Tel: 31 317 485 254 Fax: 31 317 484 254 Email: Geert.Smant@wur.nl, nema.wau.nl, Makedonka.Dautova@medew.nema.wau.nl		
FEATURES	Location/Qualifiers 1. .556 /organism="Meloidogyne incognita" /mol_type="mRNA" /db_xref="taxon:63006" /clone="3739" /dev_stage="second stage preparasitic juveniles (J2)" /clone_lib="Meloidogyne incognita J2 (#MD99-11", /note="Vector: pMAKI; Site_1: Sfi I A; Site_2: Sfi I B; CDS III oligo dT 30 (Clontech), and Superscript II reverse transcriptase (Life Technology). cDNA clones were size fractionated directly ligated in the Sfi I A restriction site at 5', end and Sfi I B at 3', end of pMAKI. pMAKI was derived from the plasmid pCDNA 3.1 (Invitrogen)."		
BASE COUNT	161 a 113 c 124 g 158 t		
ORIGIN			
source	Query Match 29.8%; Score 511.8; DB 10; Length 556; Best Local Similarity 99.1%; Pred. No. 1, 1e-113; Mismatches 2; Indels 3; Gaps 546; Conservative 0; Mismatches 2; Indels 3; Gaps 546; Matches 994		
Qy	CAAGGAGTTACTCAATTTCACITGTCGGCAAAGCTGAGAGTATCCTCATAGTTACCTTCTTC		
Db	9 CAAGGAGTTACTCAATTTCACITGTCGGCAAAGCTGAGAGTATCCTCATAGTTACCTTCTTC		
Qy	1054 TTAAATGGTGTGAGAAGTTCATGTTCAATTCCAAGTGAAGCCGTTGATGGTTCGTCACCA		
Db	69 TTAAATGGTGTGAGAAGTTCATGTTCAATTCCAAGTGAAGCCGTTGATGGTTCGTCACCA		
Qy	1114 AAAGAAAGTTGTCATATGATTAAACCAAGAAATGATGTCGCTGAGTTGCGAAAAA		
Db	128 AAAGAAAGTTGTCATATGATTAAACCAAGAAATGATGTCGCTGAGTTGCGAAAAA		
Qy	1174 ATGGTCGAGCAAATTCAGTCAGCAGGCAATTTCGGTTATCTGCACATTTCGGCCCTCT		
Db	188 ATGGTCGAGCAAATTTCAGTCAGCAGGCAATTTCGGTTATCTGCACATTTCGGCCCTCT		
Qy	1234 GACATGGTGTGACATACTGGTAATTGAACTGGCGTCAANGCAAGCTACTGAC		
Db	248 GACATGGTGTGACATACTGGTAATTGAACTGGCGTCAANGCAAGCTACTGAC		
Qy	1294 GAGGCATATGGAAATTCCTGAGAAGTATTTGAACTGCCAACTTAACTGTTCTGTGGTACT		
Db	308 GAGGCATATGGAAAGTATTTGAACTGCCAACTTAACTGTTCTGTGGTACT		
Qy	1354 TCGGATCATGGAAATTCCTGAGAAGTATTTGAACTGCCAACTTAACTGTTCTGTGGTACT		
Db	368 TCGGATCATGGAAATTCCTGAGAAGTATTTGAACTGCCAACTTAACTGTTCTGTGGTACT		

Qy	1414	ACCTGCAATTGGTCCATTACTTGTCTCCAAACATTTGTTAAATCGACTCCA	1473	Qy	788	TGATTTCTCATTATCGGTGATCTGGTCAAATTGTGAATGTTGGGTCTC	847
Db	428	ACCTGCAATTGGTCCATTACTTGTCTCCAAACATTTGTTAAATCGACTCCA	485	Db	2	TGATTTCTCATTATCGGTGATCTGGTCAAATTGTGAATGTTGGGTCTC	61
Qy	1474	CCTACTGGAGATGGAAAGAACGTCACGGCCTAACGTGATTTGCACTGTT	1533	Qy	848	ACGGTATAAGATCTTAAATGGTGGTTCCCTACCCCTAAATTCAGATTAGTGGG	907
Db	486	CCTACTGGAGATGGCAAAAGCAGCTAACGTGATTTGCACTGTT	545	Db	62	AAGGATCAAAGATCTGAGTGTGATTAACACCCAAAGATGCAAGTAGTGGG	121
Qy	1534	CTACATTAAT 1544		Qy	908	TGACCCATAACATAAAAGATTCACCATTCATCGTTATTCCACCTGTGACTCATCTA	967
Db	546	CTACATTAAT 556		Db	122	TGACTCACTACAGCAGAAATTACATTCCTCGTTTACCAAGAATTCATAAA	181
<b>RESULT 3</b>							
LOCUS	AW152739	650 bp mRNA linear EST 28-AUG-2000		Qy	968	ATGTGCTTGTGCTGATGGCTTCTCAGGAGTTACTCAATTCTACTGTGGAAACTG	1027
DEFINITION	JALSL3C100SAC	Litomosoides sigmodontis (parasitic nematode)		Db	182	ACGTTATGGCCGAGATGGTTATACAGTCCATGGAGAAACGG	241
mRNA sequence.				Qy	1028	AGAGATCCTCATGTGACCTCTCTTAAATGGTGTGAGAGTCATCCAAAGATG	1087
ACCESSION	AW152739			Db	242	AAAATATGGCAGCTCACATCTTTCACAGGGGTGTGGGAAACAAATTGGGATG	301
VERSION	AW152739.1			Qy	1088	AGAGCGCTTGTATGGTTTCCGTACACAAAGAAGTGGTACATATGATTAAACCGAAA	1147
KEYWORDS	EST.			Db	302	AAGAACGSGTGTCTGTTAGTGTACCGA--AAGTGTGACCTATGATCTGACCAAA	358
ORGANISM	Litomosoides sigmodontis			Qy	1148	TGATGCTGCTGAGTCCGAAATAATGTCGACAAATGTCGACGGCATCTT	1207
	Litomosoides sigmodontis			Db	359	TGAGCTCGACGAGTGTGCTGTAGTTATCGAACATCTCTAAAGAACATCCAT	418
Eukaryota; Metazoa; Nematoda; Spirurida; Spirarioidea;				Qy	1208	TGTTTATGTGCAATTGGTGGACATCTGGTAAATTGTGAACCTG	1267
Onchocercidae; Litomosoides.				Db	419	TGTCATGTGCAATTGGCCTGCTGATATGGTGGCATACTGGTATGTGAAGGG	478
REFERENCE	1 (bases 1 to 650)			Qy	1268	CCGTCAAAGCATGTCAGGTACTCTGACGAGGCAATTGGAAAGATTTGACATGCCAA	1327
AUTHORS	Allen, J. E., Daub, J., Giuliano, D., McDonnell, A., Lizotte-Waniecki			Db	479	CCGTGAAGCAGTGGCAACAGATATTGCTATTGGCAATATAGCATGTARGA	538
M., Taylor, D. W. and Blixter, M.				Qy	1328	CCTATAATTACCTCTCTGATTTGCTGATCTGGAAATGCTGAGATGATTGCT	1387
TITLE	Analysis of genes expressed at the infective larval stage validates			Db	539	AGACGACTACATATTGATGTTACAGATGCAATGGAAATAATGGGCC	598
utility of Litomosoides sigmodontis as a murine model for filarial				Qy	1368	CCGATGGTAGTGAACATACTGGCACATCTGGCAATTGGCCATTFACTG	1439
vaccine development.				Db	599	CAGATGGTAGCAAGCATACTGCCACACATGGCAATTGGCCATTACTGG	650
JOURNAL	Infect. Immun. 68 (9), 5454-5458 (2000)			RESULT 4			
MEDLINE	20407372			AW589077			
PUBMED	10948183			LOCUS	327 bp	mRNA	linear EST 10-MAY-2001
COMMENT	Contact: Allen JE			DEFINITION	ra08c01..Y2	Bird-Rao Meloidogyne incognita J2	Meloidogyne incognita
	Institute of Cell, Animal and Population Biology						
	University of Edinburgh, King's Buildings, West Mains Road, Edinburgh, EH9			ACCESSION	AW589077		
	3J7, UK			VERSION	1		
	Tel: +44 131 650 7014			KEYWORDS	EST.		
	Fax: +44 131 670 5450			ORGANISM	Meloidogyne incognita		
	Email: j.allen@ed.ac.uk				Eukaryota; Metazoa; Nematoidea; Chromadorea; Tylenchida; Tylenchina;		
	The Litomosoides EST dataset (including the LSC clustering				Meloidogyne incognita (southern root-knot nematode)		
	information) is available on the www at <a href="http://www.ed.ac.uk/~t11de">http://www.ed.ac.uk/~t11de</a>				Tylenchidae; Heteroderidae; Meloidogyne; Meloidogyne.		
	imbx/Litomob/LitoeESTs.html				McCarrier, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J., Wylie, T.		
PCR PRIMERS	FORWARD: T7PL (CTCACTATAGGGAAATTGGS)				Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.		
	BACKWARD: M13 Forward (CGCCAGGTCTTCACAGTCAGC)				Gibbons, M., Ritter, E., Franklin, J., Tsagareishvili, R.		
	Seq. primer: SAC (GGAAACAAAAGCTGGAG).				Ronko, I., Kennedy, S., McGuire, L., Beck, C., Underwood, K., Steptoe		
FEATURES	Location/Qualifiers				M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.		
source	1.	organism="Litomosoides sigmodontis"			Shin, T., Jackson, Y., Cardens, M., McCann, R., Waterston, R., and		
	/mol_type="mRNA"				Wilson, R.		
	/clone_lib="Litomosoides sigmodontis (parasitic nematode)"				The Washington Univ. Nematode EST Project, 1999		
	/dev_stage="infective L3"				Unpublished		
	/note="Litomosoides sigmodontis (parasitic nematode)"				Contact: McCarter JP		
	/note="Vector: Lambda Zap II; Site 1: EcoRI (5' end);				The Washington Univ. Nematode EST Project, 1999		
	Site 2: XbaI (3' end); Litomosoides sigmodontis is a				The Washington Univ. School of Medicine		
	filarial nematode parasite of rats. The library was				4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
	constructed from vector-(Ornithonyssus bacoti) derived L3				Tel: 314 286 1800		
BASE COUNT	202 a	126 c	152 g				
ORIGIN							
Query Match	18.7%	Score 320.8;	DB 9;				
Best Local Similarity	69.3%	Pred. No. 4.1e-57;	Length 650;				
Matches	452;	Conservative 0;	Mismatches 197;	Indels 3;	Gaps 1;		

Fax: 314 286 1810  
 Email: est@wustl.edu  
 The library was constructed by Uma Rao and David Bird  
 (david\_bird@wustl.edu) at North Carolina State University. DNA  
 Sequencing by: Washington University Genome Sequencing Center St.  
 Louis.  
 Seq primer: T3 ET from Amersham  
 High quality sequence stop: 269.  
 Location/Qualifiers  
 1. .327  
 /organism="Meloiodogyne incognita"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:63006"  
 /dev\_stage="enriched for 2nd stage juveniles"  
 /lab\_host="XLRN"  
 /clone\_lib="Bird-Rao Meloidogyne incognita J2"  
 /note="Vector: ZAP express - PBKCMV (Stratagene); Site\_1:  
 EcoRI; Site\_2: XbaI; Oligo (dT) primed library. cDNA was  
 constructed and cloned unidirectionally into the vector  
 within the 5' EcoRI and 3' XbaI sites. This library was  
 constructed by Dr. Uma Rao and Dr. David Bird at North  
 Carolina State University."  
 93 a 52 c 80 g 102 t

FEATURES	Source	National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.
	Location/Qualifiers	<code>/organism="Caenorhabditis elegans"</code> <code>/mol_type="mRNA"</code> <code>/strain="N2"</code> <code>/db_xref="taxon:6239"</code> <code>/clone="YK1152E03"</code> <code>/sex="hermaphrodite"</code> <code>/tissue_type="whole animal"</code> <code>/dev_stage="L1"</code> <code>/clone_lib="unpublished oligo-capped</code> <code>elegans L1 stage"</code>
BASE COUNT		180 a 125 c 178 g 193 t 1 o
ORIGIN		Query Match 17.5%; Score 300.8; DB 12; L Best Local Similarity 67.7%; Pred. No. 3.1e-62; Matches 435; Conservative 0; Mismatches 205; In

Query Match	17.5%	Score 301.4; DB 9; Length 327;	
Best Local Similarity	97.8%	Pred. No. 1.6e-6; Mismatches 6; Indels 1; Gaps 1;	
Matches	316;	Conservative	0;
		Mismatches	6;
		Indels	1;
		Gaps	1;
503	CAACAAGTGGAGCTGGTTATCTGAAACACTCTTCCTCAATTATGGCTCGAAAGTACG	562	Db
6	CCAACTGGGAACTGGGTTTGTGTT-CCTGAAACACTCTTCCTCAATTATGGCTCGAAAGTACG	64	Db
563	GAGAAATGGCTACTATTAATCTGGAGGTTATTATCCATGGTATGGACAAAGATGGAC	622	Qy
65	GAGAAATGGCTACTATTAATCTGGAGGTTATTATCCATGGTATGGACAAAGATGGAC	124	Db
623	GTTTAAAGATGGCTTATGGCAATTGGGCAATTGGGCAAAAGCACCCTTGTATA	682	Qy
125	GTTTAAAGATGGCTTATGGCAATTGGGCAATTGGGCAAAAGCACCCTTGTATA	184	Db
683	AGGCTGTGCGATGTTGTTAGAGAGCGATAATGCTGAACTGAGCAAAATCTGAAAC	742	Qy
185	AGGCTGTGCGATGTTGTTAGAGAGCGATAATGCTGAACTGAGCAAAATCTGAAAC	244	Db
743	CAATTGGTTTTCGGACCATGGCGATTAAGATGAGGATCTCTTCTCAATT	802	Qy
245	CAATTGGTTTTCGGACCATGGCGATTAAGATGAGGATCTCTTCTCAATT	304	Db
803	ATCGTGTGATCTATGGTCAA	825	Qy
305	ATCGTGTGATCTATGGTCAA	327	Db
RESULTS	5		
1112231	BJ112231	677 bp mRNA linear EST 23-JAN-2002	
ORGANISM	Caenorhabditis elegans	unpublished oligo-capped cDNA library; C. elegans L1 stage EST.	
DEFINITION	Caenorhabditis elegans	Caenorhabditis elegans cDNA clone ykl152e03 5', mRNA sequence.	
ACCESSION	BJ112231	G1:18272281	
SEQUENCE			
REFERENCE	1	(bases 1 to 677)	
SEQUENCE	1	TTGAGATGGCAAAATATCAAAATGTTCAACAAAAGCTGCTTGTAGTTATGTGGAT	76
SEQUENCE	26	TGGCGATGGCAAAATAACAGTTGGCCAAATAAGCTGTCATCGTATGTTATGTGGAT	85
SEQUENCE	77	GGGGCCTTTCGCGATGACAACAGGGGAATGCAATTGGCTAAAGCTAAACGCCATTATATGG	136
SEQUENCE	86	GGGGAGTTTCGAGAATCCTTACGGTACGGCTATTCTCAACGACAGAACCCAGTATGG	145
SEQUENCE	137	ACAAACTTTGGTTCTGGAATTGGCAAAATAATGGAGGACACGCGTCTCATGTTGATGTC	196
SEQUENCE	146	ACAAAGCTGTGTTGGCGCAATGGCTCAATTGGGCAATGGCATGTCATGTTGTCCTCC	205
SEQUENCE	197	CAGAAAGCCTTAATGGGAATTGTGAACTGGACATTTGAAATAGACGCTGGAGAGTTA	256
SEQUENCE	206	CAGAAGGATGATGGGAAATTCGGAACTGGGACATGGGCAATTGGGAGCTGGAGCTGTATA	265
SEQUENCE	257	TTTATCAAGATATTGTCGAATTATGTCGAATTTCACGAAACGAGTTGTTACAAATC	316
SEQUENCE	266	TCTATCAAAGATTTGTCGTTAATCTGGCAAGTCAGAACAAATTGTCATCTAG	325
SEQUENCE	317	CTCAGATTGTTGTCATCAGGTGAGCTGAGCTGAGGTTGCGATTGCAATTATTAG	376
SEQUENCE	326	AGAGCCTGGTGTGATGCCCTGGATCTGCGATCTGCTCTAAACGGAATGGACTTCACTGCGCG	385
SEQUENCE	377	GAATGGTTGGATGGTGTGTTGGCTTACCTCTCATTTGATCATCTTCTGGTGTATGCTG	436
SEQUENCE	386	GACTTGTTCGAGGAGGTGTCTATCTCATTTGATCATCTCATTTGATCTGGTTAAGG	445
SEQUENCE	437	CATTTTAAACATTACAGTCAGGCAAAAGTTCATCACTTTGGCTGATGGCGAGATA	496
SEQUENCE	446	CCATCCTAAGACTGGCTTACAGCTTCAATTCTTACCTTCATTCTACGGAGATGGCTGTATA	505
SEQUENCE	497	CTTCGCCAACAGTGGAGAATTGGCTACTATCTCTCAATTATTGCAATGGCACAATA	553
SEQUENCE	506	CTGGATATGGAAAACATGCGACTCTGTTGATTCCTGAAACACCCTCGAGTCCTGGAGAAAACATA	565
SEQUENCE	554	AAAAGTACGGGAATGGCTACTATCTCTCAATTATTGCAATGGCACAATA	613
SEQUENCE	566	CTGGATATGGAAAACATGCGACTCTGTTGATTCCTGAAACACCCTCGAGTCCTGGAGAAAACATA	625
SEQUENCE	614	GATGGAGAGCTTAAAGATGGCTTATGGAGATGGCTTATGGTGGAGG	656
SEQUENCE	626	GATGGAGAGCTTAAAGATGGCTTATGGAGATGGCTTATGGTGGAGG	658

RESULT 6  
**AU204921**  
**LOCUS** AU204921 linear DNA, *Drosophila melanogaster*, EST, 17-JUL-2001  
**655 bp**  
**mRNA**  
**VERSION** N204921  
**DEFINITION** mRNA, linear, *Drosophila melanogaster*, EST, 17-JUL-2001  
**ACCESSION** AU204921  
**VERSION** N204921  
**COMMENT**  
**TITLE** A complementary view of the *C.elegans* genome  
**JOURNAL** Unpublished  
**AUTHOR** Sugano, S.  
**CONTACT** Tadashu Shin-1  
**INSTITUTION** Center for Genome Resources, Information

ACCESSION	Caenorhabditis elegans cDNA clone yk843c10 5', mRNA sequence.	Db	507	CTCTCCAAACAGTGGAGTTGGATTCCGAAACACCTCCAGTCTGGAGAAACTA 566	
VERSION	AU204921	QY	554	AAAGTACGGAGAATTCGCTACTATTACTGGACGTTATTATGCAATGGATAGGGACAAAA 613	
KEYWORDS	EST.	Db	567	CTGGATATGGAAACTAGCTACTGTAGTGGCGCTACTATGCTATGGATCCGATAACA 626	
SOURCE	Caenorhabditis elegans	QY	614	GATGGGGCCGTATTACATGGCTATAG 642	
ORGANISM	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae	Db	627	GATGGGGCCGTATTACATGGCTATAG 655	
REFERENCE	Rhabditidae; Peledinae; Caenorhabditis				
AUTHORS	Kohara, Y., Shin-i,T., Thierry-Mieg, J., Suzuki, Y., and Sugano, S.				
TITLE	A complementary view of the C.elegans genome				
JOURNAL	Unpublished				
COMMENT	Contact: Yuji Kohara Genome Biology Lab. National Institute of Genetics Yata 111-1, Mishima, Shizuoka 411, Japan Tel: 81-559-81-6854 Fax: 81-559-81-6855 Email: ykohara@lab.nig.ac.jp.				
FEATURES	Location/Qualifiers 1. 655 /organism="Caenorhabditis elegans" /mol_type="mRNA" /strain="N2" /db_xref="taxon:6239" /clone="y-843c10" /sex="Hermaphrodite" /tissue_type="whole animal" /dev_stage="L4" /clone_id="unpublished oligo-capped cDNA library, stage L4"				
BASE COUNT	175 a 124 c 169 g 187 t				
ORIGIN					
Query Match	17.0%	Score 292.6; DB 9; Length 655;			
Best Local Similarity	67.6%	Pred. No. 3e-60;			
Matches	425; Conservative	0; Mismatches 201; Indels 3; Gaps 1;			
QY	17	TTGAGATGGACAAATTCAAAATGTTAACACAAAATCTGCTTGTAGTTATGGAT 76	QY	17	TGAGATGGACAAATTCAAAATGTTAACACAAAATGTTCTGTAGTTATGGAT 76
Db	27	TGGGAGGGCAATAACAGTGGGCCAAATAAGGCTGCTCATGGTTATGGAT 86	Db	26	TGGGAGGGCAATAACAGTGGGCCAAATAAGGCTGCTCATGGTTATGGAT 85
QY	77	GGGCCTTTCGGATGAAACACGGGATGCAATTGCTAACGCTTAACGCCTATATGG 136	QY	77	TGAGATGGACAAATTCAAAATGTTCTGTAGTTATGGCTTAAACGGCTTATGG 136
Db	87	GGGAGGTTCTGAGATTCAGGTAACTGGCAATGGCTTACATGGTGGTTGC 146	Db	86	GGGAGGTTCTGAGATTCAGGTAACTGGCTTACATGGTGGTTGC 145
QY	137	AACAACTTGGTCTGGAAATTGGCAAGGCAACCGTCTCATGGTGGTTGC 196	QY	137	ACAAACTTGGTCTGGAAATTGGCAAGGCAACACCACTGGTCTCATGGTGGTTGC 196
Db	147	ACAGCTGTTGTTGGCAATGGCTTAATTGGCAATGGTCTCATGGTGGCTCC 206	QY	137	ACAAACTTGGTCTGGAAATTGGCAAGGCAACACCACTGGTCTCATGGTGGATTGC 196
QY	197	CAGAAGCTTAATGGAAATTGGCAATGGTCAACAAATTGGTACAAATC 256	Db	146	ACAGCTGTTGTTGGCAATGGTCTCATGGTCTCATGGTGGATTGC 205
Db	207	CAGAAGGATTGGAAATTGGCAACTGGCATGTCATGGCTCATGGCTCC 266	QY	197	CAGAAGCTTAATGGAAATTGGTCAACAAATTGGTACAAATC 256
QY	257	TTTATCAAGATATTGCGCAATTAAATTGGAGCTGGTCAACGAGTTGTGTTACAAATC 316	Db	206	CAGAAGGATTGGAAATTGGTCAACAAATTGGTACAAATC 265
Db	267	TCTATCAAGACATTGTCGTTGTTACATGGTCAACGAGTTGTGTTACAAATC 326	QY	257	TATCAAGATATTGGCAATTAAATTGGTCAACGAGTTGTGTTACAAATC 316
QY	317	CTCAGATGTTGTCATGAGCTGCGTCAAAAGGGAGTGGTGGATTTAG 376	Db	266	TCTATCAAGACATTGTCGTTGTTACATGGTCAACGAGTTGTGTTACAAATC 325
Db	327	AGAGCTTGGTGGATGGCTGGCATGTCATGGCTCATGGCTCATGGCCG 386	QY		
QY	377	GACTGGTAAAGGTTTCAATGGTCAACGAGTTGTGTTACAAATC 436	Db		
Db	387	GATGTTGTCATGGAGGTGTCATCTCATGGCTCATGGCTCATGGTAAAG 446	QY		
QY	437	CATTTAACAAATTACAGTGGCAAGGGTTTCAATGGTCAACGAGTTGTGTTACAAATC 496	Db		
Db	447	CCATCAAGAACAGTGGAGCTGGAGATTCAGGAGATGGTGGTGGTCAAC 506	QY		
QY	497	CTCGCCAAACAGTGGAGCTGGTGTATCTGACAATCTCAATTTG--CTCGG 553	Db		



Db	601	AAGAACGGAGT <sup>TT</sup> GGTCCATGCCGA	627
RESULT 10			
BQ513449	BQ513449	28 25 bp mRNA linear EST 26-JUN-2002	
LOCUS	rd0603.y1	Meloidogyne incognita egg SLL TOPO v1	Meloidogyne
DEFINITION	incognita	CDNA 5'	similar to TR:044742 044742 F57/B10.3 PROTEIN. [1]
mRNA	sequence.		
ACCESSION	BO613449		
VERSION	BQ613449.1	GI:21603118	
KEYWORDS	EST.		
SOURCE	Meloidogyne incognita (southern root-knot nematode)		
ORGANISM	Meloidogyne incognita		
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;			
Tylechtoidea; Heteroderidae; Meloidogyneinae; Meloidogyne.			
REFERENCE	1 (bases 1 to 285)		
AUTHORS	McCartor, J., Clifton, S., Chiappalli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steppoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shain, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.		
TITLE	The Washington Univ. Nematode EST Project, 1999		
JOURNAL	Unpublished		
COMMENT	Contact: McCartor, JP		
	The Washington Univ. Nematode EST Project, 1999		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: estwatson.wustl.edu		
	The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. <i>Meloidogyne incognita</i> eggs were provided by Andrew Kloek of Divergence Inc., St. Louis, MO. Putative full length read.		
	The vector to vector length is 286		
	Seq primer: -40RP from Gibco.		
FEATURES	Location/Qualifiers		
	1 .. 285		
	/organism="Meloidogyne incognita"		
	/mol_type="mRNA"		
	/db_xref="Taxon:6306"		
	/dev_stage="egg"		
	/lab_host="DH10B (Invitrogen)"		
	/clone_id="Meloidogyne incognita egg SLL TOPO v1"		
	/note="vector: pCRII-TOPO (Invitrogen); Site:1 EcorI; Site:2 EcoRI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SLL PCR based library. cDNA PCR products of size >400 nucleotides containing SLL on the 5' end and oligo(dt) on the 3' end were non-directionally cloned into pCRII-TOPO (Invitrogen) following the TOPO TA cloning protocol. <i>Meloidogyne incognita</i> eggs were provided by Andrew Kloek of Divergence Inc., St. Louis, MO."		
BASE COUNT	92 a	43 c	69 g
ORIGIN		81 t	
Query	Match	Score 278.2;	Length 285;
	Best Local Similarity	98.9%;	Pred. No. 6.8e-57;
	Matches	280;	Conservative
Qy	70	GATGGATGGGCCCTTTCGGATGAAACACGGGAATGCAATTGCTAAAGCTAAACGCCCT	129
Db	2	GATGGATGGGCCCTTTCGGATGAAACACGGGAATGCTAAAGCTAAACGCCCT	61
Qy	130	ATTATGGACAACTTGTCTGGAAATGGCAAAATGGAAACAGGGTTTCATGTT	189
Db	62	ATTATGGACAACTTGTCTGGAAATGGCAAAATGGAAACAGGGCTTCATGTT	121
Qy	190	GGATGGCCAGAAAGCCCTTAATGGGAAATTCTGAATGGACATTGGAAATATGGAGCTT	249

Db	122	GGATGCCAGAGCTTAATGGAAATTCTGAAGTGGACATTGATAGGCTGGA	181	Db	241	GATGCTTGGCATCGTGTCTCATCTGGCCGGACTCTGTTCT	300
Qy	250	AGAGTATTTATCAAGATAATTGTCGAAATTGCGCTTCACGAAACGAGTTGTT	309	Qy	388	GATGGTGGTGCACACTCTCATATGATCATCTTGGCTTGAACTGTCATTTAAACAA	447
Db	182	AGAGTATTTATCAAGATAATTGTCGAAATTGCGCTTCACGAAACGAGTTGTT	241	Db	301	GACGGAGGGTTCTCATATGATCATCTTGGCTTGAACTGTCATTTAAAGAG	360
Qy	310	ACAAATCTCAGATGTTGATCAGCTGACCGTCAAGAAAG 352		Qy	448	TTACAGTGGCAAGGTTTCATCACAATTGTCATGGTCAAGATCTGCCAACAA	507
Db	242	ACAAATCTCAGATGTTGATCAGCTGACCGTCAAGAAAG 284		Db	361	CTCGGAGGTTCCAGACTTACCTTCATCCAGGAGTGTCTGATCTCCAAAC	420
RESULT 11				Qy	508	AGTGGAGCCTGTTATCTGAACAACTCTTCATGTTGAGGAAACTACTGGATATGGA	564
LOCUS	BJ116367	580 bp mRNA linear	EST 23-JAN-2002	Db	421	AGTGGAGTGGATGATCAGCTGAGTCTGGAGAAAACACTGGATATGGA	480
DEFINITION	BJ116367	unpublished oligo-capped cDNA library, C. elegans L1 stage		Qy	565	GAATTGGCTACTATTACTGGACATTATTGCAATGGGACAAAAGATGGAGCGT	624
ACCESSION	BJ116367	Caenorhabditis elegans cDNA clone yk1202d10 5', mRNA sequence.		Db	481	AAACTAGCTGCTGACTGATGGATGCGATAACAGATGGAGCGT	540
VERSION	BJ116367.1	GI:18276478		Qy	625	ATTAAAGATGGCTTATGAGGCAATTGTTGAGGATTGGGA	663
KEYWORDS				Db	541	ATCACATGTCATACGANECAATTGTTGGCTGTTGGA	579
ORGANISM	Caenorhabditis elegans			RESULT 12			
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae				BJ107746	623 bp mRNA linear	EST 23-JAN-2002	
; Rhabditidae; Peioderinae; Caenorhabditis.				LOCUS	BJ107746	unpublished oligo-capped cDNA library, C. elegans L1 stage	
REFERENCE	1	(bases 1 to 580)		DEFINITION	Caenorhabditis elegans cDNA clone yk1100a07 5', mRNA sequence.		
AUTHORS	Kohara,Y., Shin-i,T., Thierry-Mieg,J., Suzuki,Y.			ACCESSION	BJ107746		
TITLE	A complementary view of the C.elegans genome			VERSION	BJ107746.1		
COMMENT	1	(bases 1 to 580)		SOURCE	EST.		
CONTACT	Tadasu Shin-i			ORGANISM	Caenorhabditis elegans		
National Institute of Genetics				Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidae			
1111 Yata, Mishima, Shizuoka 411-8540, Japan				Rhabditidae; Peioderinae; Caenorhabditis.			
Tel: 81-559-81-6855				1 (bases 1 to 623)			
Fax: 81-559-81-6855				REFERENCE	Kohara,Y., Shin-i,T., Thierry-Mieg,J., Suzuki,Y.		
Email: tshini@genes.nig.ac.jp.				AUTHORS	and Sugano,S.		
FEATURES	1.	580		TITLE	A complementary view of the C.elegans genome		
source	/organism="Caenorhabditis elegans"			JOURNAL	Unpublished		
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	/strain="N2"				Center For Genetic Resource Information		
	/db_xref="taxon:6239"				National Institute of Genetics		
	/clone="yk1202d10"				1111 Yata, Mishima, Shizuoka 411-8540, Japan		
	/sex="hermaphrodite"				Tel: 81-559-81-6856		
	/tissue_type="whole animal"				Fax: 81-559-81-6855		
	/dev_stage="L1"				Email: tshini@genes.nig.ac.jp.		
	/clone_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"			FEATURES	Location/Qualifiers		
BASE COUNT	155	a 111 c 150 g 163 t 1 others		source	1.		
ORIGIN					1.	623	
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Query Match	16.1%	Score 277.2; DB 12; Length 580;		BASE COUNT	165	a 119 c 159 g 180 t	
Best Local Similarity	68.6%	Pred. No. 1.6e-56;		ORIGIN			
Matches	397;	Conservative 0; Mismatches 179; Indels 3; Gaps 1;		Query Match	15.9%	Score 272.8; DB 12; Length 623;	
				Best Local Similarity	67.1%	Pred. No. 2e-55;	
				Matches	401; Conservative 0; Mismatches 194; Indels 3; Gaps 1;		
Qy	88	GATGACAAACACGGGATGCAATGCTAAAGCTTAAATTGGACAAACACTTGT	147	Qy	17	TGGAGATGGACAATTAACATGCTTCAACAAAAGCTTCACATGGCTTGTAGTTATGATGGAT	76
Db	1	GAAGATCCCTACGGCTCAAAATGGGCTTCAACGGCAGACGAGCTTGT	60	Db	26	TGGCGATGCCAAATTAACAGTTCGGCTGGCAATAGGTCTGTCATCGTTATGATGGAT	85
Qy	148	TCTGGAAATTGGCAAATTGGGACACGGCTTCAATGGTGGATGCCAGAGGCTTA	207	Qy	181	ATGGTTCGTTAAATCTGCAATGGCTTCAACGACAAATTGTCGTTAGTGTGAGCTTGT	136
Db	61	TCGGGCAATTGGGCTCAAAATGGGCAATGGCTTCAATGGCTGGTGT	120	Db	86	GGGAGTTCTGGAGATCCTAACGGTAACTGGCTGCAATGGCTTCAACGACAGACACAGTTATG	145
Qy	208	ATGGGAAATTCTGAAATTGGGACACGGCTTCAATGGTGGATGCCAGAGGCTTA	267	Qy	328	GCATCAGCTGAGCTGCAAAGGGGAGTGGCTGATGCAATTAGACTGGTTAGC	387
Db	121	ATGGGAAATTCTGCAATGGCTTCAACGGCTTCAATGGCTGGTGT	180	Db			
Qy	268	ATGGTTCGTTAAATCTGCAATGGCTTCAACGACAAATTGTCGTTAGTGTGAGCTTGT	240				
Db	181	ATGGTTCGTTAAATCTGCAATGGCTTCAACGACAAATTGTCGTTAGTGTGAGCTTGT	387				
Qy							



/strain="N2"		ORGANISM	Caenorhabditis elegans
/db_xref="taxon:6239"		Eukaryota; Metazoa; Nematoda; Chronadorea; Rhabditida; Rhabditoidea	
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/sex="hermaphrodite"		1 (bases 1 to 621)	
/tissue_type="whole animal"		Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.	
/dev_stage="L1"		and Sugano, S.	
/clone_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"		A complementary view of the C. elegans genome	
BASE COUNT	187 a 155 c 165 g 212 t 7 others	COMMENT	Unpublished
ORIGIN		CONTACT	Tadasu Shin-i
		Center For Genetic Resource Information	
		National Institute of Genetics	
		1111 Yata, Mishima, Shizuka 411-8540, Japan	
		Tel: 81-559-81-6856	
		Fax: 81-559-81-6855	
		Email: tshin-i@genes.nig.ac.jp	
		Location/Qualifiers	
		1. .621	
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Query Match	15.7%; Score 270.6; DB:12; Length 726;	BASE COUNT	163 a 120 c 159 g 179 t
Best Local Similarity	64.2%; Pred. No. 7.2e-55;	ORIGIN	
Matches 446; Conservative	0; Mismatches 225; Indels 24; Gaps 2;	Query Match	15.7%; Score 269.8; DB:12; Length 621;
Qy	883 CCTAAAATATTCAAGATTAGGGATGCCAAATACAAATAAGAGTTCATTCATCG 942	Best Local Similarity	68.5%; Pred. No. 1.e-54;
Db	725 CCATCAAATCTCAAGATAATGGAAATCAATACAAAGCCGAGTCCTAACATCG 666	Matches 387; Conservatve	0; Mismatches 175; Indels 3; Gaps 1;
Qy	943 TTATTCCCACCGCAGTCATACTAATGTCGTTGCTGAGTGGCTTCAGAGT 1002	Qy	47 AAAAGTCTGCTGTAGTTATGATGGATGGCCCTTCGATGAAACAGGGAAAT 106
Db	665 CTGTTCCGCCAGATGGACAAATGTTATGGCTAGTCCTTAATGGT 606	Db	56 ATAGGCTGTCTCATCGTTATGATGGATGGAGTTCTGAGATCCTAGGTACG 115
Qy	1003 ACTCAATTCACTGTGGAAACTTGAGAAAGTATCCTCATGTTACCTCTCTTAATGGT 1062	Qy	107 CAATTGCTAAAGCTAAACGCCATTATGGACAAACTTGTGCTGGAAATTCGCCAAAAAT 166
Db	605 TCGAAATTCACTGTGGAAACCCGAAAAATCCTCACGTTACATTTCTCAATCGA 546	Db	116 CTTATCTAACGGACAGCACGGTTATGGACAGCTGTTGGGCAATGGCTCAA 175
Qy	1063 GGTGAGAAGTTCAATTCCAAGATGAAAGCCTGTTCCGTACCAAAAGAATT 1122	Qy	167 TGGAAAGCACCGTCCTCATGTTGATGCCAGAAGGCTTAATGGAAATTCTGAATSTG 226
Db	545 GGACTTGAACAACTTGGGNAAGAAGCTGTTAGTGGCCATCAAATGATCAA 489	Db	176 TTTAGGGACATCTCTCATGTTGCTTCATGTTGGCTTCACAGGGAAATTCGGAA 235
Qy	1123 GCTACATGATTAAACCAAGAATGAAATGCTGCTGAGTGGAAATGGTCGAG 1182	Qy	227 GACATTGAAATAGGAGCTGGAGAGTTATTCATGAGATTTGTCGAATTAAATTGG 286
Db	488 GCAACTTAGATCTCACCGAGGATCCTTGGTTATGTGCAATTGGCTCTGCATGGT 1242	Db	236 GACATTGAAACATGGAGCCGGCGCTGGTTATCATCACACATGTTCATGGT 295
Qy	1183 CAAATTGAGTCAGGCGGGATCCTTGGTTATGTGCAATTGGCTCTGCATGGT 1242	Qy	287 CTGTTCAACGAAACGAGTTGTTACAATCCCTGAGATTTGTCGATCACGTCAGT 346
Db	428 CAACTCGAGGCTGAAACTCATCCATTATGTGCAACTTGTGTCACCAAGATGTC 369	Db	296 CAGTCAGAACACAAATTGTGACTTGTGAGGCTTGGCTGATGTCGTTGCTA 355
Qy	1243 GGACATACGTGTTAAATTGCAACCTGCTCAAGCTACATGTCAGCGGGCAATT 1302	Qy	347 AGAAGGGAGTGTGCTGATTGCTGATGTTAGGATGTGGTGTGTCACCTCTC 406
Db	368 GGCAATACGGAGGNTATGAGCTGTCAGGCTGAGTGGCTGAAACACTGTCACATGTAC 309	Db	356 AAACGGAAATGACGTGCTTCACATGGGGACTTGTGAGGAGGTGTCATCTC 415
Qy	1303 GGAAGAGATATTGAGACATGCCAAACCTATAATTAGCTGTTATGTTACTTCGATAT 1362	Qy	467 TCAATTCACTTTGCTGATGGGAGTGGCTGAGATCTCCGATTTGTCGTTGCTG 526
Db	308 GGAAGATCTATGAGACAACTCAAGACGGGAACTCANTATGGTACTGTGTAC 249	Db	476 ACCTTCATTTCTGAGGAGATGGCTGATACTCTCCTCCAGTGGATTCCTG 535
Qy	1363 GGAATGCTGAGAGATGATGCTGCTCCAGTGGTAGTGAACATACTGCACATACCTGGAT 1422	Qy	527 AACACCTCTCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
Db	248 GGAATGCTGAAAGATGAGGGCTCAGATGGCTGAAACACACTGTCACACATGTAC 189	Db	536 AACAAACCTCTGAGTTGGAGAAAACACTGCTGCTGCTGCTGCTGCTGCTG 595
Qy	1423 TTGGTCCATTACTTGTGCTCTCCAAACATGCTGCTCCTACCTTGGA 1482	Qy	584 GACGTTATTATGCAATGGATAGGGA 608
Db	188 CGTGTCTCCACTACTTGTGCTCCTACCTTGGA 150	Db	596 GCGCTACTATGCTGATGTCCTCGGA 620
Qy	1483 GATGATGGAAAGAACGTCAGCCATTGATGGTGTGACCTGACGACTGTTCAACATTA 1542	RESULT 15	
Db	149 GTCGATCCAGCCGACCGTCATCGCCCTTGTGATGTTGCTCCACCTACTGGA 90	Qy	BJ117851
Qy	1543 ATGGGTCTTACCTGTACCGCGGAGATGGATGGGGT 1577	LOCUS	BJ117851
Db	89 ATGGGACTCCCTCAACAGCTGAAATGACTGGGGT 55	DEFINITION	unpublished oligo-capped cDNA library, C. elegans L1 stage
		VERSION	EST
		KEYWORDS	Caenorhabditis elegans
		SOURCE	



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